

Serial Number: 09/724,693A

CRF Processing Date: 2/14/2001

Edited by: [Signature]

Verified by: [Signature]

(STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_

- ☐ Added the mandatory heading and subheadings for "Current Application Data".

- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_

- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_

- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_

- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_

- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_

- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_

- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_

- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_

- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_

- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_

- ☒ Other: Seq 8 - corrected amino acid nos.

**RECEIVED**

**FEB 20 2001**

**TECH CENTER 1600/2900**

1 Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING                      DATE: 02/14/2001  
PATENT APPLICATION:    US/09/724,693A        TIME: 10:38:17

Input Set : A:\Pto.amc  
Output Set: N:\CRF3\02142001\I724693A.raw

## SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:  
6        (i) APPLICANT: Hadlaczky, Gyula  
7                      Szalay, Aladar  
C--> 9        (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF  
10                      AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES  
12        (iii) NUMBER OF SEQUENCES: 34  
14        (iv) CORRESPONDENCE ADDRESS:  
15                      (A) ADDRESSEE: Heller Ehrman White & McAuliffe  
16                      (B) STREET: 4250 Executive Square, 7th Floor  
17                      (C) CITY: La Jolla  
18                      (D) STATE: CA  
19                      (E) COUNTRY: USA  
20                      (F) ZIP: 92037  
22        (v) COMPUTER READABLE FORM:  
23                      (A) MEDIUM TYPE: Diskette  
24                      (B) COMPUTER: IBM Compatible  
25                      (C) OPERATING SYSTEM: DOS  
26                      (D) SOFTWARE: FastSEQ Version 1.5  
28        (vi) CURRENT APPLICATION DATA:  
C--> 29                      (A) APPLICATION NUMBER: US/09/724,693A  
C--> 30                      (B) FILING DATE: 28-Nov-2000  
50                      (C) CLASSIFICATION:  
C--> 47        (vii) PRIOR APPLICATION DATA:  
33                      (A) APPLICATION NUMBER: 08/835,682  
34                      (B) FILING DATE: 10-APR-1997  
38                      (A) APPLICATION NUMBER: 08/695,191  
39                      (B) FILING DATE: 07-AUG-1996  
43                      (A) APPLICATION NUMBER: 08/682,080  
44                      (B) FILING DATE: 15-JUL-1996  
48                      (A) APPLICATION NUMBER: 08/629,822  
49                      (B) FILING DATE: 10-APR-1996  
52        (viii) ATTORNEY/AGENT INFORMATION:  
53                      (A) NAME: Seidman, Stephanie L  
54                      (B) REGISTRATION NUMBER: 33,779  
55                      (C) REFERENCE/DOCKET NUMBER: 24601-402G  
58        (ix) TELECOMMUNICATION INFORMATION:  
59                      (A) TELEPHONE: 858-450-8403  
60                      (B) TELEFAX: 858-587-5360  
61                      (C) TELEX:  
63 (2) INFORMATION FOR SEQ ID NO: 1:  
65        (i) SEQUENCE CHARACTERISTICS:  
66                      (A) LENGTH: 1293 base pairs  
67                      (B) TYPE: nucleic acid  
68                      (C) STRANDEDNESS: single  
69                      (D) TOPOLOGY: linear  
71        (ii) MOLECULE TYPE: Genomic DNA

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72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
76      (ix) FEATURE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80  GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT      60
81  TCTCGCCATA TTCTGGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT      120
82  TTCGTCAATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN      180
83  GCCATATTTC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTT AGTTTTCTCTC      240
84  GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC      300
85  CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA      360
86  TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
87  ATTCATGTGC CTACAATGAT CATTTTAAAT TTCCACCTT TTCATTTTTC CACGCCATAT      480
88  TTCAATGTCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTCTT CGCCATATTC      540
89  CAGGTCCTAC AGTGTGCATT CCTCATTTT   CACCTTTTTT ACTGATTTCT TCATTTTTC      600
90  AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTTCAG TTATCTTGTC ATATTCCATG      660
91  TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTGACG      720
92  TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
93  CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCAAT TTTTCCAGTT      840
94  GTCAAGGGGA TGTTCCTCAT TTTCCATGAG TGTCAGTTT   CTTGCTATAT TCCATGTCCT      900
95  ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTTC TCACCATATT TCACGTCCTA      960
96  AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA      1020
97  GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT      1080
98  GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
99  ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTCATCGGC ACATTTACAG TCCTAAAGTG      1200
100 TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
101 CATTTCTCAT TTTTACGTT TTTTCAGTGA TTC      1293
103 (2) INFORMATION FOR SEQ ID NO: 2:
105      (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 1044 base pairs
107          (B) TYPE: nucleic acid
108          (C) STRANDEDNESS: single
109          (D) TOPOLOGY: linear
111      (ii) MOLECULE TYPE: Genomic DNA
112      (iii) HYPOTHETICAL: NO
C--> 113      (iv) ANTI-SENSE: NO
W--> 114      (v) FRAGMENT TYPE:
115      (vi) ORIGINAL SOURCE:
116      (ix) FEATURE:
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120  AGGCCTATGG TGAAAAGGA AATATCTTCC CCTGAAACT AGACAGAAGG ATTCTCAGAA      60
121  TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTTT GATAGAGCAG      120
122  TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC      180
123  CGTTGGAAAC GGGATGTGCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240
124  TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA      300
125  ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTGGAGC GATCTCAGGA CTGCGGTGAA      360
126  AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT      420
127  GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTGT AAACACTCTT      480

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128 TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCTGTTGG GAAACGGGAT 540
129 TACATATAAA AAGCAGACAG CAGCATTTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG 600
130 TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT 660
131 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
132 AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT 780
133 GAAGCTTTCT TTTGATAGAG GCAGTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
134 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
135 CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTGAA CATTCCCTTT 960
136 CAGAGAGCAG GTTTGAACAC TCTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
137 CAGGGGGGAT CCTCTAGAAT TCCT 1044
141 (2) INFORMATION FOR SEQ ID NO: 3:
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH: 2492 base pairs
145 (B) TYPE: nucleic acid
146 (C) STRANDEDNESS: single
147 (D) TOPOLOGY: linear
149 (ii) MOLECULE TYPE: Genomic DNA
150 (iii) HYPOTHETICAL: NO
C--> 151 (iv) ANTI-SENSE: NO
W--> 152 (v) FRAGMENT TYPE:
153 (vi) ORIGINAL SOURCE:
154 (ix) FEATURE:
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
158 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG 60
159 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
160 GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
161 GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
162 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GCCTTGGGGT 300
163 TGCTATCCTG GGGTTCAACC CCCCAGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
164 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAACC ATGCCAAGAG 420
165 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
166 AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
167 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
168 TTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
169 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
170 GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
171 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
172 GGGTTAGGTT TTGGGGTGCC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
173 AGACTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTAAA AGAGTTTAGC AATTCTAACA 960
174 GATATAGACC AGCTGTGCTA TCTCATGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
175 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
176 CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTAGTTT TAATAATTTT TTATATATTT 1140
177 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
178 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
179 TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAATTC ATTACCAAAC CCAAAGGCAG 1320
180 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
181 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTT CGTCTATATC CATATCATTT 1440
182 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
183 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560

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184 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
185 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
186 GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTG ACTCTGCAAT AAAAATGTCA 1740
187 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
188 CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
189 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTG 1920
190 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
191 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
192 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
193 GCTGTTTAAT GCATCGCTCA GTCCCCTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
194 CTGTGTTTCT TTTCATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
195 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
196 TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
197 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG 2400
198 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
199 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG                                     2492
201 (2) INFORMATION FOR SEQ ID NO: 4:
203     (i) SEQUENCE CHARACTERISTICS:
204         (A) LENGTH: 28 base pairs
205         (B) TYPE: nucleic acid
206         (C) STRANDEDNESS: single
207         (D) TOPOLOGY: linear
209     (ii) MOLECULE TYPE: Genomic DNA
210     (iii) HYPOTHETICAL: NO
C--> 211     (iv) ANTI-SENSE: NO
W--> 212     (v) FRAGMENT TYPE:
213     (vi) ORIGINAL SOURCE:
214     (ix) FEATURE:
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218 GGGGAATTCA TTGGGATGTT TCAGTTGA                                     28
220 (2) INFORMATION FOR SEQ ID NO: 5:
222     (i) SEQUENCE CHARACTERISTICS:
223         (A) LENGTH: 29 base pairs
224         (B) TYPE: nucleic acid
225         (C) STRANDEDNESS: single
226         (D) TOPOLOGY: linear
228     (ii) MOLECULE TYPE: Genomic DNA
229     (iii) HYPOTHETICAL: NO
C--> 230     (iv) ANTI-SENSE: NO
W--> 231     (v) FRAGMENT TYPE:
232     (vi) ORIGINAL SOURCE:
233     (ix) FEATURE:
235     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA                                     29
239 (2) INFORMATION FOR SEQ ID NO: 6:
241     (i) SEQUENCE CHARACTERISTICS:
242         (A) LENGTH: 47 base pairs
243         (B) TYPE: nucleic acid
244         (C) STRANDEDNESS: single

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RAW SEQUENCE LISTING                                DATE: 02/14/2001
PATENT APPLICATION:  US/09/724,693A                 TIME: 10:38:17

Input Set : A:\Pto.amc
Output Set: N:\CRF3\02142001\I724693A.raw

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245      (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
248      (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250      (v) FRAGMENT TYPE:
251      (vi) ORIGINAL SOURCE:
252      (ix) FEATURE:
254      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC
260 (2) INFORMATION FOR SEQ ID NO: 7:
262      (i) SEQUENCE CHARACTERISTICS:
263          (A) LENGTH: 25 base pairs
264          (B) TYPE: nucleic acid
265          (C) STRANDEDNESS: single
266          (D) TOPOLOGY: linear
268      (ii) MOLECULE TYPE: Genomic DNA
269      (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271      (v) FRAGMENT TYPE:
272      (vi) ORIGINAL SOURCE:
273      (ix) FEATURE:
275      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTTTAAAT TAATTAAGCC CGGGC
280 (2) INFORMATION FOR SEQ ID NO: 8:
282      (i) SEQUENCE CHARACTERISTICS:
283          (A) LENGTH: 27 base pairs
284          (B) TYPE: nucleic acid
285          (C) STRANDEDNESS: single
286          (D) TOPOLOGY: linear
288      (ii) MOLECULE TYPE: Genomic DNA
289      (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291      (v) FRAGMENT TYPE:
292      (vi) ORIGINAL SOURCE:
293      (ix) FEATURE:
295      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTTTAAAT TAATTCGGGC CCGTCGA
299 (2) INFORMATION FOR SEQ ID NO: 9:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 69 base pairs
303          (B) TYPE: nucleic acid
304          (C) STRANDEDNESS: single
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: Genomic DNA
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
314 1          5          10          15
316 GTC ACA AAC AGT GCA CCT ACT

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## VERIFICATION SUMMARY

DATE: 02/14/2001

PATENT APPLICATION: US/09/724,693A

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\02142001\I724693A.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1  
L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1  
L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2  
L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2  
L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3  
L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3  
L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4  
L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4  
L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5  
L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5  
L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6  
L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7  
L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8  
L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]  
L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:  
L:340 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]  
L:434 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:439 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11  
L:435 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11  
L:453 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:458 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12  
L:454 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12  
L:472 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:473 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13  
L:513 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:514 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14  
L:554 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:555 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15  
L:594 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:980 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:981 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17  
L:1714 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1715 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18  
L:1735 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1736 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19  
L:1765 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1766 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20  
L:1790 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1791 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21  
L:1814 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1815 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22  
L:1838 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1839 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23  
L:1867 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1868 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24  
L:1897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1898 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25  
L:1915 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1916 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26  
L:1933 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1934 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27  
L:1951 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1952 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28  
L:1969 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1970 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29  
L:1988 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:1989 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30  
L:2006 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2007 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31  
L:2024 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2025 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32  
L:2042 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2043 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33  
L:2060 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]  
L:2061 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34